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#15

RAW SEQUENCE LISTING

DATE: 05/08/2002

PATENT APPLICATION: US/09/000,004A

TIME: 10:40:08

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1 <110> APPLICANT: Tsilibary, Photini-Effie
 2 Charonis, Aristidis S.
 3 Setty, Suman
 4 Mauer, Michael
 5 <120> TITLE OF INVENTION: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC
 NEPHROPATHY
 6 <130> FILE REFERENCE: 600.314USWO
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/000,004A
 8 <141> CURRENT FILING DATE: 2001-06-19
 9 <150> PRIOR APPLICATION NUMBER: US 60/001,387
 10 <151> PRIOR FILING DATE: 1995-07-21
 11 <150> PRIOR APPLICATION NUMBER: US 60/001,861
 12 <151> PRIOR FILING DATE: 1995-08-03
 13 <150> PRIOR APPLICATION NUMBER: US 60/016,700
 14 <151> PRIOR FILING DATE: 1996-05-02
 15 <150> PRIOR APPLICATION NUMBER: PCT/US96/12067
 16 <151> PRIOR FILING DATE: 1996-07-19
 17 <160> NUMBER OF SEQ ID NOS: 16
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 3989
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Rattus
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (420)..(3959)
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 32 tgtggcaatc catctgggat gtgagacgcg tggagagggc ttagcagcat ttgacaaaaa 240
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 35 ttcttgccag ctctgccc cgaaccggca cgtagctggt tccagcagcc gctccagca 419
 36 atg gtc ccc agg cgt cct gcc agc cta gag gtc act gta gcc tgc ata 467
 37 Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
 38 1 5 10 15
 39 tgg ctt ctc acg gtc atc cta ggc ttc tgc gtc tcc ttc aat gtt gat 515
 40 Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
 41 20 25 30
 42 gtg aaa aac tca atg agt ttc agt ggc cca gta gag gac atg ttt gga 563
 43 Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
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46	Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile	
47	50 55 60	
48	ggt tct cct tta gtt ggc caa ccc aaa gca aga act gga gat gtc tat	659
49	Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr	
50	65 70 75 80	
51	aag tgt ccg gtt ggg aga gag aga gca atg cct tgc gtg aag ttg gac	707
52	Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp	
53	85 90 95	
54	ttg cca gtt aac aca tcg atc ccc aat gtc aca gaa ata aag gaa aac	755
55	Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn	
56	100 105 110	
57	atg aca ttt gga tca act tta gtc acc aac ccg aat gga gga ttt ctg	803
58	Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu	
59	115 120 125	
60	gca tgt ggg ccc ttg tat gcc tat aga tgt gga cat ttg cat tat aca	851
61	Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr	
62	130 135 140	
63	act gga ata tgt tct gat gtc agt cct aca ttt caa gtt gtg aac tcc	899
64	Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser	
65	145 150 155 160	
66	ttt gcc cct gta caa gaa tgc agc acc cag ctg gac ata gtc atc gtc	947
67	Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val	
68	165 170 175	
69	ctg gat ggc tcc aac agc atc tac ccc tgg gaa agt gtc atc gcc ttt	995
70	Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe	
71	180 185 190	
72	tta aac gac ctt ctt aag agg atg gat att ggc cct aag cag aca cag	1043
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75	gtc ggg att gta cag tat gga gag aat gta acc cat gag ttc aac ctc	1091
76	Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu	
77	210 215 220	
78	aat aag tat tca tcc aca gaa gag gtc ctt gtc gca gca aac aaa ata	1139
79	Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile	
80	225 230 235 240	
81	ggc cga cag gga ggc ctc caa acg atg aca gcc ctt gga ata gac aca	1187
82	Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr	
83	245 250 255	
84	gcc agg aaa gag gca ttc act gaa gct cgg ggt gcc agg agg gga gtt	1235
85	Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val	
86	260 265 270	
87	aaa aaa gtc atg gtt att gtg acc gac gga gaa tcg cat gac aac tat	1283
88	Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr	
89	275 280 285	
90	cgc ctg aaa cag gtc atc caa gac tgc gag gac gaa aac att cag cga	1331
91	Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg	
92	290 295 300	
93	ttt tcc ata gct atc ctt ggc cac tat aac agg ggg aac tta agc act	1379

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96	gaa aaa ttt gtg gag gaa ata aaa tcg atc gca agc gag ccc acg gaa	1427
97	Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu	
98	325 330 335	
99	aag cac ttc ttc aat gtc tcg gat gag ttg gcc ctg gtc act att gtt	1475
100	Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val	
101	340 345 350	
102	aaa gct ctg gga gaa agg ata ttc gct ttg gaa gcg aca gct gac cag	1523
103	Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln	
104	355 360 365	
105	tca gca gct tca ttt gag atg gaa atg tct cag act ggc ttc agt gct	1571
106	Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala	
107	370 375 380	
108	cac tac tcc cag gac tgg gtc atg ctt gga gcg gtg gga gcc tat gac	1619
109	His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp	
110	385 390 395 400	
111	tgg aac gga act gtg gtc atg cag aag gct aac cag atg gtc atc cct	1667
112	Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro	
113	405 410 415	
114	cat aac acc acc ttt caa act gag ccc gcc aag atg aac gag cct ctg	1715
115	His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu	
116	420 425 430	
117	gct tct tat tta ggt tac aca gtg aac tcg gcc acc atc cct gga gat	1763
118	Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp	
119	435 440 445	
120	gtg ctc tac atc gct ggg cag cct cgg tac aat cat acg ggc cag gtc	1811
121	Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val	
122	450 455 460	
123	gtc atc tac aag atg gag gat ggg aac atc aac att ctg cag aca ctc	1859
124	Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu	
125	465 470 475 480	
126	ggc gga gag cag att ggt tcc tac ttt ggt agt gtc tta aca aca att	1907
127	Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile	
128	485 490 495	
129	gac atc gac aaa gat tct tat act gat ctg ctt ctc gtc ggg gcc ccc	1955
130	Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro	
131	500 505 510	
132	atg tac atg ggg aca gag aaa gag gaa cag ggc aag gtg tac gtg tac	2003
133	Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr	
134	515 520 525	
135	gct gtg aat cag aca agg ttt gaa tat caa atg agc ctg gaa cca att	2051
136	Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile	
137	530 535 540	
138	agg cag acc tgc tgc tca tcc ctg aag gat aat tca tgc acg aaa gaa	2099
139	Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu	
140	545 550 555 560	
141	aac aag aat gag ccc tgc ggg gcc cgc ttc gga aca gca att gct gct	2147
142	Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala	

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145	Val	Lys	Asp	Leu	Asn	Val	Asp	Gly Phe Asn Asp Val Val Ile Gly Ala
146			580			585		590
147	ccg	ctg	gaa	gat	gac	cac	gca	gga gct gtg tac att tat cat ggc agt 2243
148	Pro	Leu	Glu	Asp	Asp	His	Ala	Gly Ala Val Tyr Ile Tyr His Gly Ser
149			595			600		605
150	ggc	aag	acc	ata	agg	gag	gcg	tat gca caa cgc att cca tca ggt ggg 2291
151	Gly	Lys	Thr	Ile	Arg	Glu	Ala	Tyr Ala Gln Arg Ile Pro Ser Gly Gly
152		610				615		620
153	gat	ggc	aag	acc	ctg	aaa	ttt	ttc ggc cag tct atc cac gga gag atg 2339
154	Asp	Gly	Lys	Thr	Leu	Lys	Phe	Phe Gly Gln Ser Ile His Gly Glu Met
155		625				630		635
156	gat	tta	aat	ggt	gac	ggt	ctg	act gac gtg acc att gga ggc ctt ggt 2387
157	Asp	Leu	Asn	Gly	Asp	Gly	Leu	Thr Asp Val Thr Ile Gly Gly Leu Gly
158				645				650
159	gga	gca	gcc	ctc	ttc	tgg	gcc	aga gat gtg gct gta gtt aaa gtg acc 2435
160	Gly	Ala	Ala	Leu	Phe	Trp	Ala	Arg Asp Val Ala Val Val Lys Val Thr
161			660					665
162	atg	aat	ttt	gaa	ccc	aat	aaa	gtg aat att caa aag aaa aac tgc cgt 2483
163	Met	Asn	Phe	Glu	Pro	Asn	Lys	Val Asn Ile Gln Lys Lys Asn Cys Arg
164			675					680
165	gtg	gag	ggc	aaa	gaa	aca	gtg	tgc ata aat gct aca atg tgt ttt cat 2531
166	Val	Glu	Gly	Lys	Glu	Thr	Val	Cys Ile Asn Ala Thr Met Cys Phe His
167		690						695
168	gtg	aaa	tta	aag	tct	aaa	gag	gac tca att tac gag gct gat ctg cag 2579
169	Val	Lys	Leu	Lys	Ser	Lys	Glu	Asp Ser Ile Tyr Glu Ala Asp Leu Gln
170		705						710
171	tac	cgt	gtc	acc	ctt	gat	tca	ctg agg cag ata tca cgg agc ttt ttt 2627
172	Tyr	Arg	Val	Thr	Leu	Asp	Ser	Leu Arg Gln Ile Ser Arg Ser Phe Phe
173				725				730
174	tct	gga	act	cag	gaa	agg	aag	att caa aga aat atc acc gtt cga gaa 2675
175	Ser	Gly	Thr	Gln	Glu	Arg	Lys	Ile Gln Arg Asn Ile Thr Val Arg Glu
176			740					745
177	tca	gaa	tgc	atc	agg	cac	tcc	ttc tac atg ttg gac aaa cat gac ttt 2723
178	Ser	Glu	Cys	Ile	Arg	His	Ser	Phe Tyr Met Leu Asp Lys His Asp Phe
179			755					760
180	cag	gac	tct	gtg	aga	gtg	act	ctg gat ttt aat ctc act gat cca gaa 2771
181	Gln	Asp	Ser	Val	Arg	Val	Thr	Leu Asp Phe Asn Leu Thr Asp Pro Glu
182		770						775
183	aat	ggt	cct	gta	ctt	gat	gac	gct ctg cca aac tca gtc cac gaa cac 2819
184	Asn	Gly	Pro	Val	Leu	Asp	Asp	Ala Leu Pro Asn Ser Val His Glu His
185		785						790
186	att	ccc	ttt	gcc	aaa	gac	tgt	gga aac aag gaa aga tgc att tca gac 2867
187	Ile	Pro	Phe	Ala	Lys	Asp	Cys	Gly Asn Lys Glu Arg Cys Ile Ser Asp
188			805					810
189	ctc	act	ctg	aat	gtg	tcc	acc	aca gaa aag agc ctg ctg atc gtc aag 2915
190	Leu	Thr	Leu	Asn	Val	Ser	Thr	Thr Glu Lys Ser Leu Leu Ile Val Lys
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195	gac agt gcg tac aac acc agg aca gtg gtg cag cat tca cca aat ctg	3011
196	Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu	
197	850 855 860	
198	att ttt tcg gga att gag gag atc caa aaa gat agc tgt gaa tct aat	3059
199	Ile Phe Ser Gly Ile Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn	
200	865 870 875 880	
201	caa aat atc act tgc aga gtt gga tat cct ttc cta aga gca gga gaa	3107
202	Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu	
203	885 890 895	
204	acg gtt acc ttc aaa ata ata ttc cag ttt aac aca tcc cat ctc tcg	3155
205	Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser	
206	900 905 910	
207	gaa aat gca atc att cac tta agt gca aca agt gac agt gag gag ccc	3203
208	Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro	
209	915 920 925	
210	ctg gaa tct ctt aat gat aat gaa gta aat att tcc atc cca gta aaa	3251
211	Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys	
212	930 935 940	
213	tat gaa gtt gga ctg cag ttt tac agt tct gcg agt gaa cat cac att	3299
214	Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile	
215	945 950 955 960	
216	tca gtc gct gcc aat gag acg atc cct gag ttt att aac tcc act gag	3347
217	Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu	
218	965 970 975	
219	gac att ggg aat gaa att aat gtc ttc tat acg att aga aag agg ggg	3395
220	Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly	
221	980 985 990	
222	cat ttc cca atg cca gaa ctt cag ctg tca att tca ttc ccc aat ttg	3443
223	His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu	
224	995 1000 1005	
225	acg gca gat ggt tat cct gta ctg tac cca att gga tgg tca tct	3488
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227	1010 1015 1020	
228	tca gat aat gtg aac tgt aga ccc cgg agc ctt gag gac ccc ttt	3533
229	Ser Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe	
230	1025 1030 1035	
231	ggc atc aac tct ggg aag aaa atg aca ata tcg aag tct gag gtt	3578
232	Gly Ile Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val	
233	1040 1045 1050	
234	ctc aaa aga ggc aca atc cag gac tgc agt agt acg tgt gga gtt	3623
235	Leu Lys Arg Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val	
236	1055 1060 1065	
237	gcc acc atc acg tgt agc ctc ctt cct tcc gac ctg agt caa gtg	3668
238	Ala Thr Ile Thr Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val	
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240	aat gtc tcg ctc ctc ctg tgg aaa ccg act ttc ata aga gca cat	3713

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L:7 M:270 C: Current Application Number differs, Wrong Format